UNITED STATES PATENT AND TRADEMARK OFFICE

UNITED STATES DEPARTMENT OF COMMERCE
United States Patent and Trademark Office
Address: COMMISSIONER FOR PATENTS
P.O. Box 1450
Alexandria, Virginia 22313-1450
www.uspto.gov

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/644,594	08/19/2003	Tony N. Frudakis	DNA1170-2	6207

28213 7590 03/28/2011

DLA PIPER LLP (US)
4365 EXECUTIVE DRIVE
SUITE 1100
SAN DIEGO, CA 92121-2133

EXAMINER	
WHALEY, PABLO S	

ART UNIT	PAPER NUMBER
1631	

MAIL DATE	DELIVERY MODE
03/28/2011	PAPER

Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

Office Action Summary	Application No.	Applicant(s)	
	10/644,594	FRUDAKIS ET AL.	
	Examiner	Art Unit	
	PABLO WHALEY	1631	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE *3* MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *08 February 2011*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1,84-100 and 102-115* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1, 84-100, and 102-115* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date *2/8/2011*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____.
5) ☐ Notice of Informal Patent Application
6) ☐ Other: _____.

DETAILED ACTION

Request For Continued Examination

A request for continued examination under 37 CFR 1.114, including the fee set forth in 37 CFR 1.17(e), was filed in this application after final rejection. Since this application is eligible for continued examination under 37 CFR 1.114, and the fee set forth in 37 CFR 1.17(e) has been timely paid, the finality of the previous Office action has been withdrawn pursuant to 37 CFR 1.114. Applicant's submission filed on 02/08/2011 has been entered.

Applicant's arguments, filed 02/08/2011, have been fully considered.

The following rejections and/or objections are either reiterated or newly applied. They constitute the complete set presently being applied to the instant application.

Applicants have amended their claims, filed 02/08/2011, and therefore rejections newly made in the instant office action have been necessitated by amendment.

Status of Claims

Claims 2-83 and 101 are cancelled. Claims 1, 84-100, and 102-115 are pending and under consideration.

Information Disclosure Statement

The IDS filed 02/08/2011 has been considered in full.

Priority

The priority claims to a series of non-provisional and provisional applications are acknowledged.

Claim rejections - 35 USC § 112, 2nd Paragraph

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.
>
> The essential inquiry pertaining to this requirement is whether the claims set out and circumscribe a particular subject matter with a reasonable degree of clarity and particularity. Definiteness of claim language must be analyzed, not in a vacuum, but in light of: (A) The content of the particular application disclosure; (B) The teachings of the prior art; and (C) The claim interpretation that would be given by one possessing the ordinary level of skill in the pertinent art at the time the invention was made.

Claims 1, 84-100, and 102-115 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. Claims that depend directly or indirectly from claim 1 are also rejected due to said dependency.

Claim 1 (step f) recites: (ii) determining a likelihood of all possible proportional affiliations among four ancestral groups having the greatest likelihood values, whereby a population structure that correlates with the nucleotide occurrences of the SNPs detected in the test individual is identified. This limitation is confusing for several reasons. Which ancestral groups is this limitation referring to? Those in the two-way, three-way, or four-way comparison? Clarification is requested. Furthermore, the "whereby" phrase is confusing. Is this intended to be an active method step, a further limitation of the population structure (e.g. limiting data), or something else? This

rejection could be overcome, for example, by amending the claim to recite "correlating population structure with nucleotide occurrences."

Claims 89 and 90 limit the second populations of SNPs to comprise SEQ ID NOs: 1 to 331. Claim 97 limits the second populations of SNPs to comprise SEQ ID NOs 1 to 71. It is unclear whether claims 89, 90 and 97 are intended to limit the second population to comprise ALL the recited SEQ ID's; or to comprise ONE (or a plurality of) oligonucleotide(s) selected from the group consisting of the recited sequences. Clarification is requested. In light of the specification, which discloses that a second population may comprise ONE or more hybridizing nucleotides (para 75), and that a kit may comprise two or more panels of oligonucelotides (which correspond to the first and second populations of the methods), wherein each panel comprises as few as five members (para 182), or as few as two (para 184), the claims are interpreted as limiting the second population to comprise one or more oligonucleotides selected from the group consisting of the recited SEQ ID NO's.

Applicant is cautioned that a second population comprising ALL of SEQ ID NO's 1-331 may be new matter. Support is found in the original spec. for a FIRST population/panel comprising all of SEQ ID NO's 1-331 (para 182) or 1-71 (par's 32), but not for a SECOND population/panel comprising the same sequences. Support is found in para 79 for a second panel comprising "at least five" oligonucleotides specific for AIMs, as set forth in SEQ ID NO's 1-71, thus a second panel/population comprising all of SEQ ID No's 1-71 would not be considered new matter. No such support is found for a SECOND panel or population comprising ALL of SEQ ID NO's 1-331. However, as

the claims are interpreted to be directed to a second population comprising one or more oligonucleotides selected from the group consisting of..., (i.e. wherein the selected group may be less than the entirety of SEQ ID No's 1-331), the claims are not rejected at this time for reciting new matter.

Claim Rejections - 35 USC § 103

Response to Arguments

Applicant's arguments, filed 02/08/2011, have been fully considered but are not persuasive for the following reasons.

In response to applicant's argument that Parra teaches away from the claimed invention because Parra teaches prior knowledge of ancestral groups that is not required by the claimed invention, "the prior art's mere disclosure of more than one alternative does not constitute a teaching away from any of these alternatives because such disclosure does not criticize, discredit, or otherwise discourage the solution claimed...." In re Fulton, 391 F.3d 1195, 1201, 73 USPQ2d 1141, 1146 (Fed. Cir. 2004). See also MPEP §2123. Furthermore, Parra teaches a method for inferring the extent of European admixture in six different African-American populations [See Abstract], which reads on a method of inferring proportional ancestry. Therefore, the examiner maintains that the combination of references teaches and/or makes obvious the claimed limitations.

In response to applicant's argument that Parra, Cargill, and Shriver do not teach large numbers of samples for determining BGA proportions, the claims do not recite any

limitations directed to testing a particular size of a patient population, nor any specific limitation regarding a "large" number of samples.

In response to applicant's argument that the claimed invention results in an unexpected advantage in light of Example 2 of the specification, the MPEP Section 716.01(c) states that unexpected results must be established by factual evidence. The example (pages 104-112) is essentially comparing 4-way admixture tests with 3-way admixture tests. There are no metrics presented that show measureable improvement or unexpected results using the claimed invention. There is no data comparing applicant's method with those of the closest prior art, showing that the claimed method results in an unexpected advantage. Due to the absence of such tests, applicant's assertion of unexpected results constitutes mere argument. See also In re Linder, 457 F.2d 506, 508, 173 USPQ 356, 358 (CCPA 1972; Ex parte George, 21 USPQ2d 1058 (Bd. Pat. Appl. & Inter. 1991).

For these reasons, the examiner maintains that the combination of references teaches and/or makes obvious the claimed limitations. However, the rejections have been modified to address newly added limitations.

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains.

> Patentability shall not be negatived by the manner in which the invention was made.
>
> This application currently names joint inventors. In considering patentability of the claims under 35 U.S.C. 103(a), the examiner presumes that the subject matter of the various claims was commonly owned at the time any inventions covered therein were made absent any evidence to the contrary. Applicant is advised of the obligation under 37 CFR 1.56 to point out the inventor and invention dates of each claim that was not commonly owned at the time a later invention was made in order for the examiner to consider the applicability of 35 U.S.C. 103(c) and potential 35 U.S.C. 102(e), (f) or (g) prior art under 35 U.S.C. 103(a).

The factual inquiries set forth in *Graham* **v.** *John Deere Co.*, 383 U.S. 1, 148 USPQ 459 (1966), that are applied for establishing a background for determining obviousness under 35 U.S.C. 103(a) are summarized as follows:

1. Determining the scope and contents of the prior art.
2. Ascertaining the differences between the prior art and the claims at issue.
3. Resolving the level of ordinary skill in the pertinent art.
4. Considering objective evidence present in the application indicating obviousness or nonobviousness.

Claims 1, 84-86, 91-96, 98-100, and 104-109 are rejected under 35 U.S.C. 103(a) as being unpatentable over Parra et al. (Am. J. Physical Antropol., January 2001, Vol. 114, Issue 1, p. 18-29), in view of Cargill et al. (Nature Genetics, 1999, Vol. 22, p.231-238), and in view of Shriver et al. (American Journal of Human Genetics, 1997, Vol. 60, p.957-964; IDS filed 5/20/2004).

The amended claims are now drawn to a method of inferring, with a predetermined level of confidence, proportional ancestry of at least two ancestral groups of a test individual by identification of a population structure comprising:

a) determining single nucleotide polymorphisms (SNPs) for a first population and identifying a first population of SNPs having a frequency differential (delta) > 0.4 between one or more pairs of population groups wherein the first population of SNPs are identified from a database in silico;

b) contacting a parental sample nucleic acid with one or more hybridizing nucleic acids corresponding the first population of SNPs, wherein the one or more hybridizing nucleic acids selectively hybridize to the nucleic acid in the parental sample;

c) selecting SNPs hybridizing in step (b) to generate a second population of SNPs which have a minor allele frequency > 1% and (delta) > 0.4 for at least one pair of the at least two population groups, wherein at least one of the second population of SNPs is a SNP which may be correlated with but not linked to a gene-linked trait, wherein the second population of SNPs is an autosomal marker, and wherein the at least one SNP of the second population of SNPs is not located within a region of a gene encoding a protein;

d) contacting a sample comprising nucleic acid molecules of a test individual with at least 20 second population of SNPs, wherein the second population of SNPs are indicative of a population structure, and wherein the population structure is correlated with a trait of the test individual;

e) determining the nucleotide occurrences of the second population of SNPs in the sample from the test individual;

f) identifying the population structure indicated by the nucleotide occurrences determined for the test individual, wherein identifying the population structure infers the proportional ancestry of the test individual. The population structure is identified by (i) performing six two-way comparisons, three three-way comparisons, or one four-way comparison among ancestral groups; (ii) determining a likelihood of all possible proportional affiliations among ancestral groups having the greatest likelihood values. The method identifies population structures that correlate with nucleotide occurrences of the SNPs detected in the test individual; and a single proportional combination of maximum likelihood, and g) the above information is provided to a user.

Parra teaches a method for inferring the extent of European admixture in six different African-American populations [See Abstract]. In particular, Parra teaches a method for identifying a population structure by determining SNP markers for a first population using a battery of autosomal markers (both linked and unlinked) [See Abstract, and p.19-20, DNA Analysis Section, and Table 1]. Parra identifies allele frequencies corresponding to the 10 autosomal markers have frequency differentials > 0.4 between one or more populations [Table 1, last column], which meets the claim limitation of part (c). The method requires standard PCR genotyping procedure, which inherently requires contacting parent samples with markers [See p.20, Col. 1 and Table 1, last column]. In this population of markers, at least one is an autosomal polymorphism marker (D11S429) [p.20, Col. 1, and Table 1] that is associated with ancestry [Table 5], which shows the use at least one autosomal SNP that may be correlated but not linked to a gene-trait. A combination of SNP markers are selected to

obtain an estimate of admixture for a sub-population [p.21, Col. 1, ¶ 2, and Fig. 1], wherein allele frequencies of the SNP markers are > 1% [Table 1], which is a teaching for minor allele frequencies. Parra shows the use of markers that are unlinked to certain loci [p.20, Col. 1, and p.23, Col. 2]. Parra calculates the frequency differences between populations based on SNPs [p.23, Col. 2]. The admixture distribution of the non-parental test populations is inferred within a predetermined confidence interval [p. 21 and Table 2]. Parra also shows fitting genotype frequencies to Hardy-Weinberg proportions and suggest the selection of genetic markers that show homogeneity with Africa and Europe based on allele frequency [p.20, Statistical Analysis]. Parra discloses a biogeographical ancestry trait (BGA) [Fig. 1], and admixture proportions of samples estimated using maximum likelihood calculations [p.20, Col. 2, ¶2 and ¶3].

Parra does not specifically teach limitations directed to performing six 2-way, three 3-way, or one 4-way comparison between ancestral groups, as in claim 1. However, Parra suggest this limitation by teaching statistical comparisons between three ancestral groups [Fig. 1], and statistical comparisons of markers between a plurality of different populations [see e.g. Tables 1, 3, and 4]. Therefore, Parra makes obvious performing multiple 2-way, 3-way, or 4-way comparisons between ancestral groups.

Parra determines the admixture of each individual using maximum likelihood methods and between ancestral groups [page 21, col. 2, last ¶ through page 22, col. 1, and p.25, Col. 2, and Figure 1], which reads on determining likelihood of proportional affiliations and single proportion combinations of maximum likelihood. Parra shows

population structure correlated to the occurrence of SNPs detected in the various populations (expressed as percentages) [Table 1 and Fig. 1], which reads on population structures that correspond to SNPs.

Parra does not teach a first population of SNPs identified from a database in silico, as in claim 1.

Parra does not teach selecting SNPs from a first population to generate a second population of SNPs wherein the at least one SNP of the second population of SNPs have minor allele frequencies >1% and are not located within a region of a gene encoding a protein, as in claim 1.

Parra does not teach performing a likelihood determination of proportional affiliations among four ancestral groups having the greatest likelihood values, whereby a population structure correlates with nucleotide occurrences of SNPs detected in the test individual, as in claim 1.

Parra does not teach performing a likelihood determination for affiliation with an East Asian ancestral group, as in claim 98.

Cargill teaches a method for screening samples to determine whether identified SNPs are coding or non-coding SNPs using well known genotyping techniques [p.232-233, Results, Table 1, and Table 2]. The method includes collecting gene sequence data from known public databases and suggests construction of comprehensive SNP databases to improve screening [See p. 237, Methods and p.236, Col. 1st paragraph]. Cargill also determines the distribution of minor allele frequency, wherein SNPs are

classified according to whether minor allele frequency is high (>15%), medium (5-15%), or low (<1%) [p.234, Col. 1, last ¶, and Col. 2, and Fig. 1], which meets the claim limitation of minor allele frequencies > 1%.

Shriver teaches a method for determining ethnic affiliations using genetic markers and likelihood analysis [Abstract and p.964, Discussion]. In particular, Shriver presents population specific alleles (PSAs) [p.957, Col. 2], as well as methods for calculating allele-frequency differentials between test samples of different populations [p.958, Col. 2]. Shriver teaches calculating likelihood values for different loci [Table 1, and Table 2]. Shriver performs two-way and three-way comparisons between multiple populations [Fig. 1-4] and suggests similar markers could be developed for the identification of other populations [p.963, last ¶, Col. 1], including those of Asian origin [p.963, last ¶, Col. 1].

It would have been obvious to one of ordinary skill in the art at the time of the instant invention to modify the method of Parra by selecting a first population of SNPs identified from a database in silico, as in claim 1, since Parra suggests genetic markers are easily obtained [p.20, Col. 1] and since Cargill shows computational methods for collecting gene sequence data from known public databases and suggests construction of comprehensive SNP databases [See p. 237, Methods and p.236, Col. 1st paragraph]. The motivation would have been to improve screening genotyping analysis by using comprehensive databases containing data from many ethnic groups, as suggested by Cargill [p.236, Col. 1st paragraph].

It would have been obvious to one of ordinary skill in the art at the time of the instant invention to modify the method of Parra by screening the first population of SNPs to generate a second population of SNPs wherein the at least one SNP of the second population of SNPs is not located within a region of a gene encoding a protein, as in claim 1, since Cargill shows screening genetic samples to determine whether identified SNPs are coding or non-coding SNPs that occur outside of the coding regions of a gene [p.232-233, Results, Table 1, and Table 2]. The motivation would have been to obtain the most informative SNP markers by screening the set of identified SNPs for non-coding SNPs which are known to affect biological function [Cargill, p.236, Col. 1, last paragraph].

It would have been obvious to one of ordinary skill in the art at the time of the instant invention to have modified the method of Parra by determining a likelihood of all possible proportional affiliations among four ancestral groups having the greatest likelihood values, with a reasonable expectation of success, since one skilled in the art would have been able to determine proportional affiliations amongst any finite number of ancestral groups using likelihood analysis with predictable results, as suggested by Shriver [Abstract and p.964, Discussion, Table 1, and Table 2] and since Shriver teaches likelihood values from three groups and suggests expanding this analysis to include additional groups [p.963, last ¶, Col. 1]. The motivation would have been to allow for the confident determination of ethnicity in forensic settings, as suggested by Shriver [Abstract and p.964, Discussion, Table 1, and Table 2].

It would have been obvious to one of ordinary skill in the art at the time of the instant invention to modify the method made obvious by Parra and Shriver by performing a likelihood determination for affiliation with an East Asian ancestral group with a reasonable expectation of success, since Shriver identifies genetic markers using likelihood analysis [Abstract and p.964, Discussion, Table 1, and Table 2] and suggests markers for those of Asian ancestry [p.963, last ¶, Col. 1]. The motivation would have been to allow for the confident determination of ethnicity in forensic settings, as suggested by Shriver [Abstract and p.964, Discussion, Table 1, and Table 2].

Claims 87-90, 97, and 110-115 are rejected under 35 U.S.C. 103(a) as being unpatentable over Parra et al. (Am. J. Physical Antropol., January 2001, Vol. 114, Issue 1, p. 18-29), in view of Cargill et al. (Nature Genetics, 1999, Vol. 22, p.231-238), and in view of Shriver et al. (American Journal of Human Genetics, 1997, Vol. 60, p.957-964; IDS filed 5/20/2004), as applied to claims 1, 84-86, 91-96, 98-100, and 104-109, above, and further in view of Sorenson et al. (US 2003/0172065; Filed Mar. 29, 2002) and in view of NCBI Database (Accession Number: NW_925173.1, 1997, pages 1-3).

Parra, Cargill, and Shriver make obvious the method of inferring ancestry, as set forth above.

Parra, Cargill, and Shriver do not teach contacting samples with at least 100 and at least 200 SNPs, as in claims 87- 88.

Parra, Cargill, and Shriver do not teach contacting samples with SEQ IDs selected from SEQ ID Nos 1-331 or 1-71, as in claims 89, 90, and 97.

Parra, Cargill, and Shriver do not teach proportional ancestries comprising a photo of a person from whom the known proportional ancestry was determined, as in claims 110-115.

Sorenson discloses a genealogical research and record keeping system for identifying commonalities in haplotypes from biological samples [Abstract]. In particular, Sorenson teaches thousands of known genetic markers and millions of characterized SNPs that can be used in analysis [see e.g. 0042 and Fig. 4] for identifying a population structure [0032, 0046-0047]. Sorenson also discloses genetic records of human eye, hair and skin color, height and other physical characteristics [0009], and ancestral data stored on microfiche and on a number of other electronic media formats including the internet [0003], which is a teaching for digital information and pictures.

NCBI Database teaches Homo sapiens chromosome 11 genomic contig, which is 100% identical to SEQ ID No. 1, as in claims 89, 90, and 97.

It would have been obvious to one of ordinary skill in the art at the time of the instant invention to have modified the method made obvious by Parra, Cargill, and Shriver by contacting samples with at least 100 or at least 200 SNPs, with a reasonable expectation of success, since one skilled in the art would have been able to use thousands of known genetic markers and millions of SNPs with predictable results, as shown by Sorenson [0042, Fig. 4]. The motivation would have been to identify previously unknown biological relationships, as suggested by Sorenson [0013, 0015].

It would have been obvious to one of ordinary skill in the art at the time of the instant invention to have modified the method made obvious by Parra, Cargill, and Shriver by using additional types of data, such as a photo of a person from whom the known proportional ancestry was determined, with a reasonable expectation of success, since the use of ancestral data stored on microfiche and in electronic media format was known in the art, as shown by Sorenson [0003, 0009], which reads on photos. The motivation would have been to improve the sharing of ancestral data using electronic formats that are suitable for the internet, as suggested by Sorenson [0003].

It would have been obvious to one of ordinary skill in the art at the time of the instant invention to have modified the method made obvious by Parra, Cargill, and Shriver by contacting samples with SEQ IDs selected from SEQ ID Nos 1-331 or 1-71, with a reasonable expectation of success, in view of the NCBI Database, which shows that at least one of these SEQ IDs was known in the art, as shown above. The motivation would have been to investigate the presence of specific human chromosomes across broad populations, as suggested by Sorenson [Abstract].

Claims 102-103 are rejected under 35 U.S.C. 103(a) as being unpatentable over Parra et al. (Am. J. Physical Antropol., January 2001, Vol. 114, Issue 1, p. 18-29), in view of Cargill et al. (Nature Genetics, 1999, Vol. 22, p.231-238), and in view of Shriver et al. (American Journal of Human Genetics, 1997, Vol. 60, p.957-964; IDS filed 5/20/2004), as applied to claims 1, 84-86, 91-96, 98-100, and 104-109, above, and further in view of Pritchard et al. (Theoretical Population Biology, 2001, Vol. 60, p. 227-237).

Parra, Cargill, and Shriver make obvious the method of inferring ancestry, as set forth above.

Parra, Cargill, and Shriver do not teach generating a graphical representation of the comparison of three ancestral groups, wherein the representation comprises a confidence contour, as in claims 102 and 103.

Pritchard teaches a method for inferring proportional ancestry of different ancestral groups in a population structure using a graphical display format [Fig. 1], as in claims 102 and 103. Points in the extreme corners of the triangular plots are correctly classified [Fig. 1], which shows groups represented in a vertex of a triangle. Ancestry is also represented using a line plot, wherein dashed lines represent individuals from a population with the most divergent allele frequencies [Fig. 1 and p.232, Col. 2], which suggests a contour indicating a level of confidence. Pritchard also teaches a computer-based program STRUCTURE for estimating population structure for 20 data sets of 50, 200, and 1000 biallelic markers [p. 232, Results].

It would have been obvious to one of ordinary skill in the art at the time of the instant invention to practice the method made obvious by Parra, Cargill, and Shriver by generating a graphical representation, with a reasonable expectation of success, since one skilled in the art would have been able to graphically represent comparisons between multiple ancestral results, such as using a triangular format taught by Pritchard [Fig. 1], with predictable results. The motivation would have been to generate user

friendly graphs for inferring ancestry in a plurality of populations, as suggested by Pritchard [Fig. 1].

Conclusion

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Pablo Whaley whose telephone number is (571)272-4425. The examiner can normally be reached between 11am-7pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Marjorie Moran can be reached at 571-272-0720. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Pablo S. Whaley
Patent Examiner
Art Unit 1631

/PW/

/Marjorie Moran/

Supervisory Patent Examiner, Art Unit 1631